



SEQUENCE LISTING

<110> Yen-Potin, Frances
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<120> Apolipoprotein A-IV-related Protein: Polypeptide, Polynucleotide
Sequences and Biallelic Markers Thereof

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<141> 2001-04-25

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<150> US 60/141,032
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<150> US 09/469,099
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			85					90					95		
Lys	Leu	Lys	Glu	Glu	Ile	Arg	Arg	Glu	Leu	Glu	Glu	Leu	Arg	Ala	Arg
		100						105					110		
Leu	Leu	Pro	His	Ala	Thr	Glu	Val	Ser	Gln	Lys	Ile	Gly	Asp	Asn	Val
		115					120					125			

```

Arg Glu Leu Gln Gln Arg Leu Gly Pro Phe Thr Gly Gly Leu Arg Thr
 130                      135                      140

Gln Val Asn Thr Gln Val Gln Gln Leu Gln Arg Gln Leu Lys Pro Tyr
145                      150                      155                      160

Ala Glu Arg Met Glu Ser Val Leu Arg Gln Asn Ile Arg Asn Leu Glu
                      165                      170                      175

Ala Ser Val Ala Pro Tyr Ala Asp Glu Phe Lys Ala Lys Ile Asp Gln
                      180                      185                      190

Asn Val Glu Glu Leu Lys Gly Ser Leu Thr Pro Tyr Ala Glu Glu Leu
 195                      200                      205

Lys Ala Lys Ile Asp Gln Asn Val Glu Glu Leu Arg Arg Ser Leu Ala
 210                      215                      220

Pro Tyr Ala Gln Asp Val Gln Glu Lys Leu Asn His Gln Leu Glu Gly
225                      230                      235                      240

Leu Ala Phe Gln Met Lys Lys Gln Ala Glu Glu Leu Lys Ala Lys Ile
                      245                      250                      255

Ser Ala Asn Ala Asp Glu Leu Arg Gln Lys Leu Val Pro Val Ala Glu
                      260                      265                      270

Asn Val His Gly His Leu Lys Gly Asn Thr Glu Gly Leu Gln Lys Ser
 275                      280                      285

Leu Leu Glu Leu Arg Ser His Leu Asp Gln Gln Val Glu Glu Phe Arg
 290                      295                      300

Leu Lys Val Glu Pro Tyr Gly Glu Thr Phe Asn Lys Ala Leu Val Gln
305                      310                      315                      320

Gln Val Glu Asp Leu Arg Gln Lys Leu Gly Pro Leu Ala Gly Asp Val
                      325                      330                      335

Glu Gly His Leu Ser Phe Leu Glu Lys Asp Leu Arg Asp Lys Val Asn
                      340                      345                      350

Thr Phe Phe Ser Thr Leu Lys Glu Glu Ala Ser Gln Gly Gln Ser Gln
                      355                      360                      365

Ala Leu Pro Ala Gln Glu Lys Ala Gln Ala Pro Leu Glu Gly
 370                      375                      380

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<210> 8
<211> 396
<212> PRT
<213> Human ApoA IV

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```

<400> 8

```

Met Phe Leu Lys Ala Val Val Leu Thr Leu Ala Leu Val Ala Val Ala
 1 5 10 15
 Gly Ala Arg Ala Glu Val Ser Ala Asp Gln Val Ala Thr Val Met Trp
 20 25 30
 Asp Tyr Phe Ser Gln Leu Ser Asn Asn Ala Lys Glu Ala Val Glu His
 35 40 45
 Leu Gln Lys Ser Glu Leu Thr Gln Gln Leu Asn Ala Leu Phe Gln Asp
 50 55 60
 Lys Leu Gly Glu Val Asn Thr Tyr Ala Gly Asp Leu Gln Lys Lys Leu
 65 70 75 80
 Val Pro Phe Ala Thr Glu Leu His Glu Arg Leu Ala Lys Asp Ser Glu
 85 90 95
 Lys Leu Lys Glu Glu Ile Gly Lys Glu Leu Glu Glu Leu Arg Ala Arg
 100 105 110
 Leu Leu Pro His Ala Asn Glu Val Ser Gln Lys Ile Gly Asp Asn Leu
 115 120 125
 Arg Glu Leu Gln Gln Arg Leu Glu Pro Tyr Ala Asp Gln Leu Arg Thr
 130 135 140
 Gln Val Asn Thr Gln Ala Glu Gln Leu Arg Arg Gln Leu Thr Pro Tyr
 145 150 155 160
 Ala Gln Arg Met Glu Arg Val Leu Arg Glu Asn Ala Asp Ser Leu Gln
 165 170 175
 Ala Ser Leu Arg Pro His Ala Asp Glu Leu Lys Ala Lys Ile Asp Gln
 180 185 190
 Asn Val Glu Glu Leu Lys Gly Arg Leu Thr Pro Tyr Ala Asp Glu Phe
 195 200 205
 Lys Val Lys Ile Asp Gln Thr Val Glu Glu Leu Arg Arg Ser Leu Ala
 210 215 220
 Pro Tyr Ala Gln Asp Thr Gln Glu Lys Leu Asn His Gln Leu Glu Gly
 225 230 235 240
 Leu Thr Phe Gln Met Lys Lys Asn Ala Glu Glu Leu Lys Ala Arg Ile
 245 250 255
 Ser Ala Ser Ala Glu Glu Leu Arg Gln Arg Leu Ala Pro Leu Ala Glu
 260 265 270
 Asp Val Arg Gly Asn Leu Lys Gly Asn Thr Glu Gly Leu Gln Lys Ser
 275 280 285

Leu Ala Glu Leu Gly Gly His Leu Asp Gln Gln Val Glu Glu Phe Arg
 290 295 300

Arg Arg Val Glu Pro Tyr Gly Glu Asn Phe Asn Lys Ala Leu Val Gln
 305 310 315 320

Gln Met Glu Gln Leu Arg Gln Lys Leu Gly Pro His Ala Gly Asp Val
 325 330 335

Glu Gly His Leu Ser Phe Leu Glu Lys Asp Leu Arg Asp Lys Val Asn
 340 345 350

Ser Phe Phe Ser Thr Phe Lys Glu Lys Glu Ser Gln Asp Lys Thr Leu
 355 360 365

Ser Leu Pro Glu Leu Glu Gln Gln Gln Glu Gln Gln Gln Glu Gln Gln
 370 375 380

Gln Glu Gln Val Gln Met Leu Ala Pro Leu Glu Ser
 385 390 395

<210> 9

<211> 1388

<212> DNA

<213> Swine Apoa IV

<400> 9

gcacaggtga gctgcctgag aacctctcct ccacggagga cccagtgcag taagagacac 60
 ttccagccca gcgggagctc aggatgttcc tgaaggctgt ggtcctgagc ctggccctgg 120
 tggccgtcac cggtgcccgg gctgaggtca atgccgacca agtggctact gtgatgtggg 180
 actacttcag ccagctgggc agcaatgcca agaaggctgt ggaacatctc cagaagtctg 240
 agctcaccga gcagctcaac actctcttcc aggacaaact tggggaagtg aacacctaca 300
 cggaggacct gcagaagaag ctggtgccct ttgccacgga gctgcatgaa cgctgacca 360
 aggactcaga gaagctgaag gaggagattc gaaggagct ggaggagctg cgagcccggc 420
 tgctgcccca cgctaccgag gtgagccaga aaatcgga caacgtgcgc gagctgcagc 480
 agcgctggg gccctttacg ggagggtgc gcaccaggt caacaccag gttcagcagc 540
 tgcagcgcca gctgaagccc tacgcagagc gcatggagtc cgtgctacgg cagaacatcc 600
 gcaacctgga ggctccgtg gcaccctatg cggatgagtt caaggccaag atcgatcaga 660
 atgtggagga gctcaagggg agcctcacgc cctatgcgga ggagctcaag gccaatatcg 720
 atcagaacgt ggaggagctg cggcgagcc tggcccccta tgcgcaggac gtccaggaga 780
 agctcaacca ccagctcgag ggctggcct tccagatgaa gaagcaggca gaggagctga 840


```

aggccaagat ctcggccaat gccgacgagc tgcggcagaa gctggtgccg gtggccgaga    900
acgtgcatgg ccattctgaag ggcaacaccg aggggctgca gaagtcgctg ctggagctga    960
gaagccacct ggaccagcag gtggaggagt tccgcctcaa ggtggagccc tacggggaga    1020
ccttcaacaa agctttggtg cagcaggtgg aggatctcag gcagaagctg ggccctttgg    1080
cgggggacgt ggagggccac ctgagcttcc tggagaagga tctgagggac aaggtcaaca    1140
ccttcttcag caccctcaaa gaggaggcga gccagggcca gagccaggcc ctccctgcac    1200
aggagaaggc gcagggccct ttggagggtc gagctgcccc tggtgctccc accccacccc    1260
tgacacctgc cctgccctgc cccctgtctg tctgtctgtc ccaaagcagt tcttgtacaa    1320
acctagggat acatgtccag tggaccgtga cactacctct ccatactcaa taaagctgct    1380
gagaaact                                     1388

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```

<210> 10
<211> 1466
<212> DNA
<213> Human Apoa IV

```

```

<400> 10
agttcccact gcagcgagg tgagctctcc tgaggacctc tctgtcagct cccctgattg    60
tagggaggca tccagtgtgg caagaaactc ctccagccca gcaagcagct caggatgttc    120
ctgaaggccg tggctctgac cctggccctg gtggctgtcg ccggagccag ggctgaggtc    180
agtgtgacc aggtggccac agtgatgtgg gactacttca gccagctgag caacaatgcc    240
aaggaggccg tggaacatct ccagaaatct gaactcacc agcaactcaa tgccctcttc    300
caggacaaac ttggagaagt gaacacttac gcaggtgacc tgcagaagaa gctggtgccc    360
tttgccaccg agctgcatga acgcctggcc aaggactcgg agaaactgaa ggaggagatt    420
gggaaggagc tggaggagct gagggcccgg ctgctgcccc atgccaatga ggtgagccag    480
aagatcgggg acaacctgcg agagcttcag cagcgcctgg agccctacgc ggaccagctg    540
cgcacccagg tcaacacgca ggccgagcag ctgcgggcgc agctgacccc ctacgcacag    600
cgcatggaga gagtgtgctg ggagaacgcc gacagcctgc aggctcgtg gagggccccc    660
gccgacgagc tcaaggccaa gatcgaccag aacgtggagg agctcaaggg acgccttacg    720
ccctacgctg acgaattcaa agtcaagatt gaccagaccg tggaggagct gcgccgcagc    780
ctggctccct atgtcagga cagcaggag aagctcaacc accagcttga gggcctgacc    840

```

```

ttccagatga agaagaacgc cgaggagctc aaggccagga tctcggccag tgccgaggag      900
ctgcggcaga ggctggcgcc cttggccgag gacgtgcgtg gcaacctgag gggcaacacc      960
gaggggctgc agaagtcact ggcagagctg ggtgggcacc tggaccagca ggtggaggag     1020
ttccgacgcc ggggtggagcc ctacggggaa aacttcaaca aagccctggt gcagcagatg     1080
gaacagctca ggacgaaact gggcccccat gcgggggacg tggaaggcca cttgagcttc     1140
ctggagaagg acctgagggg caaggtcaac tccttcttca gcaccttcaa ggagaaagag     1200
agccaggaca agactctctc cctccctgag ctggagcaac agcaggaaca gcatcaggag     1260
cagcagcagg agcagggtga gatgctggcc ctttggaga gctgagctgc ccctggtgca     1320
ctggccccac cctcgtggac acctgccctg ccctgccacc tgtctgtctg tcccaaagaa     1380
gttctggtat gaacttgagg acacatgtcc agtgggaggt gagaccacct ctcaatattc     1440
aataaagctg ctgagaatct agcctc                                           1466

```

```

<210> 11
<211> 1850
<212> DNA
<213> Rat RAP3 A

```

```

<400> 11
gcatcgtgga aagcatggct gccgtcatca cctgggcact cgccctcctc tcagtgtttg      60
caactgtaca ggcgaggaag agcttctggg agtacttcgg ccagaacagc cagggcaaag     120
gcatgatggg ccagcagcag aagctggcac aggagagcct gaaaggtagc ttggagcaag     180
acctctacaa tatgaacaat ttctagaaa agctgggacc cttgagagag cctgggaagg     240
agcctcctcg gctggcacag gatccagaag gcattcggaa gcagttgcag caagagctgg     300
aggaagtgag cacacgcctg gagccctaca tggctgcaaa gcaccagcag gtcggctgga     360
acctggaggg cttgaggcag cagttgaaac cctacacggt cgagctgatg gagcaggtag     420
gcctgagcgt gcaggatctg caagaacagc tgcgcatggg gggaaaaggc accaaggccc     480
agctcctggg gggcgtggat gaggcgatga gcctgctgca ggatatgcaa agtcgagtgc     540
tgcaccatac ggaccgagtc aaagaactct tccaccctta tgcagaacgc ttggtgactg     600
gaattgggca ccatgtgcag gagctgcacc ggagtgttgc tcctcacgca gttgccagcc     660
ccgcgagact cagtcgtgct gtgcagaccc tgtcccacaa actcacacgt aaggcgaagg     720
acttgcacac cagcatccaa cgcaacctgg atcagctgcg agatgagctc agtaccttca     780

```

```

tccgtgtcag cacagacggg gcagacaaca gagactccct ggaccctcaa gctctctctg      840
acgaggtccg ccagagactc caggcttttc gacatgacac ctacctgcag atcgctgcat      900
tccactcaggc cattgaccag gagaccgagg aaatccagca ccagctggca ccacccccgc      960
ctagccacag cgccttcgct ccagagttgg gacactcaga cagtaataag gccctgagca     1020
gactgcagag cgggctggac gacctctggg aagatattgc ctatggcctt catgaccagg     1080
gccatagtca gaataaccct gagggtcact cagggttaact ctgcagctcg ttgtctggac     1140
cctgagcctt cagcatggcc taataggcag aggggtggagg gtcctgcata ctattggcga     1200
ggccaccaaa ggtgctgctg ccccaacctg tctggcctcc tcaactcccc cactcagggtg     1260
cattacactc agtaggtttg gcaaacacag cttccgggtgc tcatttgga tcctaaggag     1320
caagagtggg gtgaaggag tggggagatg gtgtgcgggg gagactgact gcaagccagt     1380
acttgaccgt tgctagaaac ctgtgtcact acaacctgga gcccggtcc tattacttca     1440
tgctgatgg tcgctgttat agtcggtcta cagaggggaa ctctgtctc ccagggttg      1500
tcatgacagc ctttgttga agagagcagg agaacatgac acgtatgatg gagtgtgtac     1560
atccctgcc a gtggtcctgc tgggggaatc agtgatggga taaatgtgtg catccctgca     1620
gtggtcctgc tgggggatca gtgatgggat ggggcagagc ccctatttcc ttagagaact     1680
ctaaccctg taaggaactg agccctctgc agtgagggct tctgaaaacc ctgtacatag     1740
caaactgtgt gccctcttca tcatgcagtc cccacctcct gattctcggg atggaactga     1800
cttttggttg gaatgaaata gacgctcatg atggaaaaaa aaaaaaaaaa     1850

```

```

<210> 12
<211> 1300
<212> DNA
<213> Rat RAP3 B

```

```

<400> 12
gcatcggtga aagcatggct gccgtcatca cctgggcact cgcctcctc tcagtgtttg      60
caactgtaca ggcgaggaag agcttctggg agtacttcgg ccagaacagc cagggcaaag     120
gcatgatggg ccagcagcag aagctggcac aggagagcct gaaaggtagc ttggagcaag     180
acctctacaa tatgaacaat ttcctagaaa agctgggacc cttgagagag cctgggaagg     240
agcctcctcg gctggcacag gatccagaag gcattcggaa gcagttgcag caagagctgg     300
aggaagtgag cacacgcctg gagccctaca tggctgcaaa gcaccagcag gtcggctgga     360

```

```

acctggaggg cttgaggcag cagttgaaac cctacacggt cgagctgatg gagcaggtag      420
gcctgagcgt gcaggatctg caagaacagc tgcgcatggt gggaaaaggc accaaggccc      480
agctcctggg gggcgtggat gaggcgatga gcctgctgca ggatatgcaa agtcgagtgc      540
tgcaccatac ggaccgagtc aaagaactct tccaccctta tgcagaacgc ttggtgactg      600
gaattgggca ccatgtgcag gagctgcacc ggagtgttgc tcctcagca gttgccagcc      660
ccgcgagact cagtcgtgct gtgcagaccc tgtcccacaa actcacacgt aaggcgaagg      720
acttgcacac cagcatccaa cgcaacctgg atcagctgct agatgagctc agtaccttca      780
tccgtgtcag cacagacggg gcagacaaca gagactccct ggaccctcaa gctctctctg      840
acgaggtccg ccagagactc caggcttttc gacatgacac ctacctgcag atcgctgcat      900
tcactcaggc cattgaccag gagaccgagg aaatccagca ccagctggca cccccccgc      960
ctagccacag cgccttcgct ccagagttgg gacactcaga cagtaataag gccctgagca     1020
gactgcagag ccggtggac gacctctggg aagatattgc ctatggcctt catgaccagg     1080
gccatagtca gaataacctt gagggtcact cagggttaact ctgcagctcg ttgtctggac     1140
cctgagcctt cagcatggcc taataggcag aggggtggagg gtccctgcata ctattggcga     1200
ggccaccaaa ggtgctgctg ccccaacctg tctggcctcc tcaactcccc cactcagggtg     1260
cattacactc agtaggtttg gcaaaaaaaaa aaaaaaaaaa                        1300

```

```

<210> 13
<211> 367
<212> PRT
<213> Rat RAP3

```

```

<400> 13

```

```

Met Ala Ala Val Ile Thr Trp Ala Leu Ala Leu Leu Ser Val Phe Ala
1           5           10           15

```

```

Thr Val Gln Ala Arg Lys Ser Phe Trp Glu Tyr Phe Gly Gln Asn Ser
          20           25           30

```

```

Gln Gly Lys Gly Met Met Gly Gln Gln Gln Lys Leu Ala Gln Glu Ser
          35           40           45

```

```

Leu Lys Gly Ser Leu Glu Gln Asp Leu Tyr Asn Met Asn Asn Phe Leu
          50           55           60

```

```

Glu Lys Leu Gly Pro Leu Arg Glu Pro Gly Lys Glu Pro Pro Arg Leu
65           70           75           80

```

Ala	Gln	Asp	Pro	Glu	Gly	Ile	Arg	Lys	Gln	Leu	Gln	Gln	Glu	Leu	Glu	
				85							90			95		
Glu	Val	Ser	Thr	Arg	Leu	Glu	Pro	Tyr	Met	Ala	Ala	Lys	His	Gln	Gln	
				100							105			110		
Val	Gly	Trp	Asn	Leu	Glu	Gly	Leu	Arg	Gln	Gln	Leu	Lys	Pro	Tyr	Thr	
				115							120			125		
Val	Glu	Leu	Met	Glu	Gln	Val	Gly	Leu	Ser	Val	Gln	Asp	Leu	Gln	Glu	
				130							135			140		
Gln	Leu	Arg	Met	Val	Gly	Lys	Gly	Thr	Lys	Ala	Gln	Leu	Leu	Gly	Gly	
				145							150			155		
Val	Asp	Glu	Ala	Met	Ser	Leu	Leu	Gln	Asp	Met	Gln	Ser	Arg	Val	Leu	
				165							170			175		
His	His	Thr	Asp	Arg	Val	Lys	Glu	Leu	Phe	His	Pro	Tyr	Ala	Glu	Arg	
				180							185			190		
Leu	Val	Thr	Gly	Ile	Gly	His	His	Val	Gln	Glu	Leu	His	Arg	Ser	Val	
				195							200			205		
Ala	Pro	His	Ala	Val	Ala	Ser	Pro	Ala	Arg	Leu	Ser	Arg	Cys	Val	Gln	
				210							215			220		
Thr	Leu	Ser	His	Lys	Leu	Thr	Arg	Lys	Ala	Lys	Asp	Leu	His	Thr	Ser	
				225							230			235		
Ile	Gln	Arg	Asn	Leu	Asp	Gln	Leu	Arg	Asp	Glu	Leu	Ser	Thr	Phe	Ile	
				245							250			255		
Arg	Val	Ser	Thr	Asp	Gly	Ala	Asp	Asn	Arg	Asp	Ser	Leu	Asp	Pro	Gln	
				260							265			270		
Ala	Leu	Ser	Asp	Glu	Val	Arg	Gln	Arg	Leu	Gln	Ala	Phe	Arg	His	Asp	
				275							280			285		
Thr	Tyr	Leu	Gln	Ile	Ala	Ala	Phe	Thr	Gln	Ala	Ile	Asp	Gln	Glu	Thr	
				290							295			300		
Glu	Glu	Ile	Gln	His	Gln	Leu	Ala	Pro	Pro	Pro	Pro	Ser	His	Ser	Ala	
				305							310			315		
Phe	Ala	Pro	Glu	Leu	Gly	His	Ser	Asp	Ser	Asn	Lys	Ala	Leu	Ser	Arg	
				325							330			335		
Leu	Gln	Ser	Arg	Leu	Asp	Asp	Leu	Trp	Glu	Asp	Ile	Ala	Tyr	Gly	Leu	
				340							345			350		
His	Asp	Gln	Gly	His	Ser	Gln	Asn	Asn	Pro	Glu	Gly	His	Ser	Gly		
				355							360			365		